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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/045,180ADATE: 06/03/2002
TIME: 12:40:19Input Set : A:\EP.txt
Output Set: N:\CRF3\06032002\J045180A.raw

3 <110> APPLICANT: Bougueleret, Lydie
4 Chumakov, Ilya
6 <120> TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA,
Composition
7 Containing Them and Applications to Diagnosis and to Therapeutic Treatment
9 <130> FILE REFERENCE: GEN-100D1
11 <140> CURRENT APPLICATION NUMBER: US 10/045,180A
12 <141> CURRENT FILING DATE: 2001-10-18
14 <150> PRIOR APPLICATION NUMBER: US 09/486,580
15 <151> PRIOR FILING DATE: 2000-02-25
17 <150> PRIOR APPLICATION NUMBER: PCT/FR98/01864
18 <151> PRIOR FILING DATE: 1998-08-28
20 <150> PRIOR APPLICATION NUMBER: FR 97/10823
21 <151> PRIOR FILING DATE: 1997-08-29
23 <160> NUMBER OF SEQ ID NOS: 12
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 4415
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
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34 <222> LOCATION: (1)..(4415)
35 <223> OTHER INFORMATION: Def-X genomic sequence
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52 <222> LOCATION: (670)..(670)
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58 <222> LOCATION: (970)..(970)
59 <223> OTHER INFORMATION: n = a, c, g, or t.
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63 <221> NAME/KEY: misc_feature
64 <222> LOCATION: (1111)..(1111)
65 <223> OTHER INFORMATION: n = a, c, g, or t.

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68 <220> FEATURE:
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70 <222> LOCATION: (1150)..(1150)
71 <223> OTHER INFORMATION: n = a, c, g, or t.
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75 <221> NAME/KEY: CAAT_signal
76 <222> LOCATION: (1711)..(1714)
77 <223> OTHER INFORMATION:
80 <220> FEATURE:
81 <221> NAME/KEY: TATA_signal
82 <222> LOCATION: (1758)..(1767)
83 <223> OTHER INFORMATION:
86 <220> FEATURE:
87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: (1780)..(1780)
89 <223> OTHER INFORMATION: n = a, c, g, or t.
92 <220> FEATURE:
93 <221> NAME/KEY: misc_feature
94 <222> LOCATION: (1836)..(1874)
95 <223> OTHER INFORMATION: Exon 1
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99 <221> NAME/KEY: misc_feature
100 <222> LOCATION: (1875)..(1880)
101 <223> OTHER INFORMATION: splice donor site
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105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (1974)..(1974)
107 <223> OTHER INFORMATION: n = a, c, g, or t.
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119 <223> OTHER INFORMATION: n = a, c, g, or t.
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124 <222> LOCATION: (2155)..(2335)
125 <223> OTHER INFORMATION: Alu insertion
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134 <220> FEATURE:
135 <221> NAME/KEY: misc_feature
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140 <220> FEATURE:

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161 <223> OTHER INFORMATION: Exon 2
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177 <221> NAME/KEY: misc_feature
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196 <222> LOCATION: (4274)..(4276)
197 <223> OTHER INFORMATION: Translation termination codon (TAA)
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203 <223> OTHER INFORMATION:
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W--> 211 cctgtgcgta acaacatcac acnccaaatt taaccagctc tccccataac agcacgctca      180
213 tgtgttactg aggaaatgcc tgtggattgg agtgtgttct gtgtgcagga ggctggtcca      240
215 ggtttcactt ctgcaggaca ctggacgttt cccaaaacca gcagactttc cccacgtgca      300

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217 cacacacccc ttctcatttt gcctctacat ccatatccac tgggcccttc aggcacctac 360
219 taatgcccta gaacctaaaa ccatcatctg gggcccagtt ccctgaatgg ccctaattctc 420
221 ttctctctgt ggaatgagtc cagtgcccac ttctccaac ggtgaaattg ctgggctgtct 480
223 acagatcagg aactcactgc ttctcatag gggcagccga cttcactgct ctgcaacagc 540
225 gaccacccct agcgaggctt gagatgcctc ttgcctcctt aagactgagg gagacgcttc 600
227 agctctcact ccactgcccc aagtccctca cagcgcggtg cctgctgcct tcacacagag 660
W--> 229 ctgcaggggg aggtcctgtg tatccggcct gctggaccag cgctgtgcac aaccctccca 720
231 tggcaacagt ggctgcccg cctgcacact gggcttgga accctcgtgt aggtatttat 780
233 tccctcagga gtgactgcat tcttttccca ttccagaaa actgatgcca ttacctcac 840
235 tatgaggagg aggaggagga ggagggtgga gagtgggtaca ttttaaaatg tgcactattc 900
237 tccctaggac tccccctcaa ataaccagg agggaccata ccagctcatt cctgtgtatc 960
W--> 239 ccaagcatan gagtaatcat cccactcatg ctgagtgtat ggtggccatt aagcctgccc 1020
241 tgaactggct ttagaacaag gtgtttgagc acacagcacc gtcttgctgc caccttgccc 1080
W--> 243 ccctcccttg tgagacctct gagacacatt naggtctcac ctaaaaatct caggatttct 1140
W--> 245 agggcccaan cggtcctaaa aaattgtcca gtctgaactc tctaagggtca agagaagagg 1200
247 tggttgctcc ctctaagaaa ccacatgttg catgtacatc cttaattccg gaaagtccaa 1260
249 caaacctgcc ctgcttagca acacaagccg aggtgggtact cctctcaccg gggcattctc 1320
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253 aggaggctgg ttcaggccat attccaaatc ctcatctgtg tgtgagtggc attcttagcc 1440
255 tagcctcctt acagggtgga tactatgata cacagccagg ctgtcccagt ggctttcaat 1500
257 attcttttgg tccagatagt tcagcctcag caccagtgtg ggcattcacag ggtcaattgt 1560
259 cttaggagtc atggagaatt catagttggt agctacctgg gcctggccag ggetgacat 1620
261 agacaaggca tccctctgtg aactcctatt ttaatgccag ctcccaaca aatttctcaa 1680
263 ctgctcttac cagcaggat ttaactact caatagaaag taaccctgaa aattaggaca 1740
W--> 265 cctgttccca aaagaccctt aaatagggga agtcccttcn ctgcttgtgc acagctgctg 1800
267 atgtggcaac atgaggcctg ggacagggga ctgtcctctg cccactctgg tagcctcacg 1860
269 tagcttaaca atctgtcagt aatacaatac aaaacttaaa ctttcatact gcggttccac 1920
W--> 271 ccaggaagct gtgttcccaa tctgaccctg gattatgggg ccacctcaga gggnacccag 1980
273 tgaggggaata ttttgccatc tgggactgtt ggttgctggg ggcagtggct atgagctcag 2040
275 ttaataaaact caagcagttt ccttccaaac acacatgtcc tacttaactg gtccaacaga 2100
W--> 277 gatgatcata ctcatangct gctaaaacat tanttttatt ttgagaaaag tctattcatg 2160
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281 ctatgttgct caagctggtc tccaactcct gggctcaagc gatcttccta ctttggcctt 2280
283 tgaagcgct gagattgcct gtgtgagcca tcatgggggc tcaactggcc actgattaat 2340
W--> 285 cagattaatt gttttttgct attgaanttg tttgacttcc ttgtatatcc ggatatttac 2400
287 ccattctaac acgtagggtt tgcaaatatt ttctctcatg ttctgtgttg ccttttctact 2460
289 cagttgatgg tttcctttgc tgtgcagggt ctttagtggt caacgcagcc ccgcttgtct 2520
291 attttccatt ttattgcctg tccctttgat gtcatagcca agaaataatt gccagatta 2580
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295 ttaggtcttc aatccattga gttgattttt gtatgtggta taagaaaaaa gaccacatgt 2700
297 atacatatct caaattctaa ggtagtatat attagacaca tacaatgtgt ctatttacac 2760
299 acattgagct gaaaataata aacatatttt tatctttcaa tcaactctat ctctatctca 2820
301 ctgaacttgt ttcacctata gcctgatgag gttgctgtcc tctctacccc agctcctata 2880
303 ggagactgct catcccctaa cctcaaaaac ccttcatga gggtgataat gcccttgaat 2940
305 cctgcaatga attagttctc tactacagtg gaattcaggt ctgttatgag ggtctggatc 3000
307 tctgaagaga agagctctca ttttcagaaa ataagcagga tttattccct gaaattactg 3060
309 aattaaatca ctgtttcgat tactttttgc aatattaaaa gtaaatattt aaacaggtaa 3120
311 aaacagaaat aatggtaggg tcccttatcat caccgtgaat tccaagctag catagacact 3180
313 aaacctagag attcacacta gaatgaaagc tgggagagca gaggagtctc agaaggatgt 3240

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315 ggaggccaat ggacacctgc aacctctcca acgaaatgcc tacctcctct cactgcagca 3300
317 tccatctctg agccttctcg cagcagagct ataaattcag cctggctcct ccgttcccac 3360
319 acatccaactc ctgctctccc tcctctcctc cagggtgacta cagttatgag gaccctcacc 3420
321 ctctctctctg cttttctcct ggtggccctt caggcctggg cagagccgct ccaggcaaga 3480
323 gctcatgaga tgccagccca gaagcagcct ccagcagatg accaggatgt ggtcatttac 3540
325 ttttcaggag atgacagctg ctctcttcag gttccagggt agagatgcca gcatgcagag 3600
327 ctacagacta gacagaagga caggagacag gctctggaat tggatctcag tggcagatgt 3660
329 cacttaggtg gctatactta acatctctgg tcctggattt tctcatatct aaatggaata 3720
331 gagaacccaaa gaaatctaag agatttttct ttctccaaaa acttgattcc aagatatgac 3780
333 tgtgaaattc actagattta agatataagg agatgctacc tagttccttc tggagccaga 3840
335 caaacaagct taagtatata ggaaaatatt tcaccctgtc tatataggag gttttagaac 3900
337 ctggagagga gcctaagaat gtgttcagggt gtgtgtgtga tgggcaggaa tgcagaaaag 3960
339 tgaagcaaag gagaatgagt ctogaatcct gtgtgaccag cactgctctg tgtattttatt 4020
341 cctattgact gagattgttt gtgctaccgg ctgtaataca gccaacatca ctcatcagcc 4080
W--> 343 aacatgtgac ttctccaaga ttccctttac caccactgc tgnaccccggt actcagtttc 4140
345 tgatgctctc tctgggtccc caggctcaac aaagggttg atctgccatt gcagagtact 4200
347 ataactgcatt tttggagaac atcttggtgg gacctgcttc atccttggtg aacgctaccc 4260
349 aatctgctgc tactaagctt gcagactaga gaaaaagagt tcataatttt ctttgagcat 4320
351 taaagggaaat tgttattctt atacctgtgc ctgatttcc tgtcctcatc ccaaataaat 4380
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357 <211> LENGTH: 453
358 <212> TYPE: DNA
359 <213> ORGANISM: Homo sapiens
361 <220> FEATURE:
362 <221> NAME/KEY: CDS
363 <222> LOCATION: (52)..(336)
364 <223> OTHER INFORMATION: Def-X coding sequence
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368 ctctgcccac tctggtagcc tcacgtagct taacaatctg tgactacagt t atg agg 57
369 Met Arg
370 1
372 acc ctc acc ctc ctc tct gcc ttt ctc ctg gtg gcc ctt cag gcc tgg 105
373 Thr Leu Thr Leu Leu Ser Ala Phe Leu Leu Val Ala Leu Gln Ala Trp
374 5 10 15
376 gca gag ccg ctc cag gca aga gct cat gag atg cca gcc cag aag cag 153
377 Ala Glu Pro Leu Gln Ala Arg Ala His Glu Met Pro Ala Gln Lys Gln
378 20 25 30
380 cct cca gca gat gac cag gat gtg gtc att tac ttt tca gga gat gac 201
381 Pro Pro Ala Asp Asp Gln Asp Val Val Ile Tyr Phe Ser Gly Asp Asp
382 35 40 45 50
384 agc tgc tct ctt cag gtt cca ggc tca aca aag ggc ttg atc tgc cat 249
385 Ser Cys Ser Leu Gln Val Pro Gly Ser Thr Lys Gly Leu Ile Cys His
386 55 60 65
388 tgc aga gta cta tac tgc att ttt gga gaa cat ctt ggt ggg acc tgc 297
389 Cys Arg Val Leu Tyr Cys Ile Phe Gly Glu His Leu Gly Gly Thr Cys
390 70 75 80
392 ttc atc ctt ggt gaa cgc tac cca atc tgc tgc tac taa gcttgagac 346
393 Phe Ile Leu Gly Glu Arg Tyr Pro Ile Cys Cys Tyr

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 85,143,670,970,1111,1150,1780,1974,2117,2133,2186,2191,2367

Seq#:1; N Pos. 4123

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L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:120
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:660
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:960
L:243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1080
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1140
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1740
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1920
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2100
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2160
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2340
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:4080